

REMARKS

Claims 40-48 are canceled without prejudice or disclaimer. Claims 3, 5-14, 16-18, 22-28 and 31-38 were previously canceled. Claims 1, 2, 4, 15, 29, 30, and 39 are amended.

Claim 1 step (b) is amended to recite the insertion of a transposon rather than insertion of a DNA fragment comprising a transposon. The feature that there must be a continuous open reading frame between the transposon border and the secretion reporter coding region is now incorporated into claim 1 step (b); support for this may be found in the original specification on page 28, lines 11-18. In addition, claim 1 is amended to address the indefiniteness rejection, as discussed below. Claim 1 is also amended to delete the term "active" to describe secretion reporter as this is redundant.

Claims 2, 30, and 39 are amended to address the indefiniteness rejection, as discussed below.

Claims 15 and 29 are amended to recite transposon instead of DNA fragment, for which currently amended claim 1 step (b) provides proper antecedent basis.

It is respectfully submitted that the present amendment presents no new issues or new matter and places this case in condition for allowance. Reconsideration of the application in view of the above amendments and the following remarks is requested.

I. The Rejection of Claims 1-4 under 35 U.S.C. 112

Claims 1-2, 4, 15, 19-21, 29-30 and 39 are rejected under 35 U.S.C. 112, as indefinite.

The Office states that claim 1 is vague and indefinite on the basis of reciting "the complete sequence of the gene..." because it is not clear what is meant by "complete sequence." Claim 1 is amended to clarify that the "complete sequence" is the "complete coding sequence of the gene..."

Claim 1 is rejected on the basis that there is insufficient antecedent basis for the term "the complete sequence." Claim 1 is amended to recite "the complete coding sequence".

The office states that claim 1 is incomplete for omitting essential structural cooperative relationships of elements because it is not clear how the gene of interest is related to the DNA fragment comprising the secretion reporter, and because it is not clear how the complete (coding) sequence of the gene of interest is determined. Claim 1 is amended to recite "inserting by in vitro transposition into a gene in said library a transposon comprising a polynucleotide encoding a promoterless and secretion signal-less secretion reporter," and to recite that the complete coding sequence is determined by additional sequencing.

Claims 30 and 39 are rejected on the basis that there is insufficient antecedent basis for the term "the complete gene of interest." Claims 30 and 39 are amended to recite "the complete coding sequence of the gene", for which there is proper antecedent basis in the currently amended claim 1.

For the foregoing reasons, Applicants submit that the claims overcome the rejections under 35 U.S.C. 112. Applicants respectfully request reconsideration and withdrawal of the rejection.

II. The Rejection of Claims 1-4, 13, 15, 19-21, 29-30 and 39 under 35 U.S.C. 103(a)

Claims 1-2, 4, 15, 19-21, 29-30 and 39 are rejected under 35 U.S.C. 103(a) as obvious over Zhang et al. or Jacobs et al. or McCarthy et al. in view of U.S. Patent No. 5,948,622 (Reznikoff et al.). The Examiner alleges that one skilled in the art would be motivated to use transposons in the methods of Zhang et al. or Jacobs et al. or McCarthy et al. because Reznikoff et al. teach a system for *in vitro* transposition, and Zhang et al., Jacobs et al. or McCarthy et al. teach method of identifying secretory genes using a promoterless and secretion signal-less sequence polynucleotide encoding a secretion reporter. This rejection is respectfully traversed.

As acknowledged by the Examiner, Zhang et al. or Jacobs et al. or McCarthy et al. do not teach the use of a DNA fragment comprising a transposon along with the secretory reporter or *in vitro* transposition. Zhang et al. or Jacobs et al. or McCarthy et al. in combination with Reznikoff et al. also do not collectively suggest a method for identifying the complete coding sequence of a gene of interest from a gene library by inserting by in vitro transposition into a gene in said library a transposon comprising a polynucleotide encoding a promoterless and secretion signal-less secretion reporter and wherein there is a continuous open reading frame between the transposon border and the secretion reporter coding region.

In particular, Reznikoff et al. clearly does not motivate an artisan to modify the methods of Zhang et al. or Jacobs et al. or McCarthy et al. to use a transposon comprising a polynucleotide encoding a promoterless and secretion signal-less secretion reporter; wherein there is a continuous open reading frame between the transposon border and the secretion reporter coding region as Reznikoff et al. discloses the use of a different system for *in vitro* transposition. Reznikoff et al. recites that "*the transposable element can include a coding region that encodes a detectable or selectable protein, with or without associated regulatory elements such as promoter, terminator, or the like.*" (col. 10, l. 47-50; emphasis added). The skilled person would not consider a "secretion signal" to be a "regulatory element," since the role of a secretion signal is post-

translational, where it marks the encoded polypeptide for transport across the cell membrane. Consequently, Reznikoff et al. does not suggest using a transposon comprising a polynucleotide encoding a promoterless and secretion signal-less secretion reporter; wherein there is a continuous open reading frame between the transposon border and the secretion reporter coding region.

Thus, based on Reznikoff et al., one skilled in the art would not be motivated to employ *in vitro* transposition using a transposon comprising a promoterless and secretion signal-less secretion reporter, wherein there is a continuous open reading frame between the transposon border and the secretion reporter coding region in any of the techniques in Zhang et al. or Jacobs et al. or McCarthy et al. as there is no suggestion in any of the cited references to use a transposon comprising in particular a promoterless and secretion signal-less secretion reporter, wherein there is a continuous open reading frame between the transposon border and the secretion reporter coding region in an *in vitro* transposition technique in a method for identifying the complete coding sequence of a gene of interest from a gene library, wherein the gene encodes a polypeptide carrying a signal sequence for secretion or partial secretion.

For the foregoing reasons, Applicants submit that the claims overcome this rejection under 35 U.S.C. 103. Applicants respectfully request reconsideration and withdrawal of the rejection.

VI. Conclusion

In view of the above, it is respectfully submitted that all claims are in condition for allowance. Early action to that end is respectfully requested. The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: December 2, 2004

Jason I. Garbell, Reg. No. 44,116
Novozymes North America, Inc.
500 Fifth Avenue, Suite 1600
New York, NY 10110
(212)840-0097